PF-0523-2 CON

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Hillman, Jennifer L.
Corley, Neil C.
Lal, Preeti

(ii) TITLE OF INVENTION: CARBAMOYL PHOSPHATE SYNTHASE HOMOLOG

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 PORTER DRIVE
(C) CITY: PALO ALTO
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: CERRONE, MICHAEL C.
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0523 US

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (650) 855-0555
(B) TELEFAX: (650) 845-4166

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 469 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1T7T01
(B) CLONE: 2045605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

```
Met Gly Thr Val His Ala Arg Ser Leu Glu Pro Leu Pro Ser Ser
                5                   10                  15
Gly Pro Asp Phe Gly Gly Leu Gly Glu Glu Ala Glu Phe Val Glu
                20                  25                  30
Val Glu Pro Glu Ala Lys Gln Glu Ile Leu Glu Asn Lys Asp Val
                35                  40                  45
Val Val Gln His Val His Phe Asp Gly Leu Gly Arg Thr Lys Asp
                50                  55                  60
Asp Ile Ile Ile Cys Glu Ile Gly Asp Val Phe Lys Ala Lys Asn
                65                  70                  75
Leu Ile Glu Val Met Arg Lys Ser His Glu Ala Arg Glu Lys Leu
                80                  85                  90
Leu Arg Leu Gly Ile Phe Arg Gln Val Asp Val Leu Ile Asp Thr
                95                  100                 105
Cys Gln Gly Asp Asp Ala Leu Pro Asn Gly Leu Asp Val Thr Phe
                110                 115                 120
Glu Val Thr Glu Leu Arg Arg Leu Thr Gly Ser Tyr Asn Thr Met
                125                 130                 135
Val Gly Asn Asn Glu Gly Ser Met Val Leu Gly Leu Lys Leu Pro
                140                 145                 150
Asn Leu Leu Gly Arg Ala Glu Lys Val Thr Phe Gln Phe Ser Tyr
                155                 160                 165
Gly Thr Lys Glu Thr Ser Tyr Gly Leu Ser Phe Phe Lys Pro Arg
                170                 175                 180
Pro Gly Asn Phe Glu Arg Asn Phe Ser Val Asn Leu Tyr Lys Val
                185                 190                 195
Thr Gly Gln Phe Pro Trp Ser Ser Leu Arg Glu Thr Asp Arg Gly
                200                 205                 210
Met Ser Ala Glu Tyr Ser Phe Pro Ile Trp Lys Thr Ser His Thr
                215                 220                 225
Val Lys Trp Glu Gly Val Trp Arg Glu Leu Gly Cys Leu Ser Arg
                230                 235                 240
Thr Ala Ser Phe Ala Val Arg Lys Glu Ser Gly His Ser Leu Lys
                245                 250                 255
Ser Ser Leu Ser His Ala Met Val Ile Asp Ser Arg Asn Ser Ser
                260                 265                 270
Ile Leu Pro Arg Arg Gly Ala Leu Leu Lys Val Asn Gln Glu Leu
                275                 280                 285
Ala Gly Tyr Thr Gly Gly Asp Val Ser Phe Ile Lys Glu Asp Phe
                290                 295                 300
Glu Leu Gln Leu Asn Lys Gln Leu Ile Phe Asp Ser Val Phe Ser
                305                 310                 315
Ala Ser Phe Trp Gly Gly Met Leu Val Pro Ile Gly Asp Lys Pro
                320                 325                 330
Ser Ser Ile Ala Asp Arg Phe Tyr Leu Gly Gly Pro Thr Ser Val
                335                 340                 345
Arg Gly Phe Ser Met His Ser Ile Gly Pro Gln Ser Glu Gly Asp
                350                 355                 360
Tyr Leu Gly Gly Glu Ala Tyr Trp Ala Gly Gly Leu His Leu Tyr
                365                 370                 375
Thr Pro Leu Pro Phe Arg Pro Gly Gln Gly Gly Phe Gly Glu Leu
                380                 385                 390
Phe Arg Thr His Phe Phe Leu Asn Ala Gly Asn Leu Cys Asn Leu
                395                 400                 405
Asn Tyr Gly Glu Gly Pro Lys Ala His Ile Arg Lys Leu Ala Glu
                410                 415                 420
Cys Ile Arg Trp Ser Tyr Gly Ala Gly Ile Val Leu Arg Leu Gly
                425                 430                 435
Asn Ile Ala Arg Leu Glu Leu Asn Tyr Cys Val Pro Met Gly Val
                440                 445                 450
Gln Thr Gly Asp Arg Ile Cys Asp Gly Val Gln Phe Gly Ala Gly
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                455                     460                     465
Ile Arg Phe Leu
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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1786 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: THP1T7T01
(B) CLONE: 2045605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

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GTCCAGGGGG TTTGTGGGAG TTGCCTTGAC CTGCAGCTCC GCCACCGCGG ACCCGCCTTC   60
TGCCCTCAGC AGCAGACGCT CTGTCCCGCC CGGGCAGCTC TGCGAGGCAG CGGCTGGAGA  120
GGGAACCATG GGGACTGTGC ACGCCCGGAG TTTGGAGCCT CTTCCATCAA GTGGACCTGA  180
TTTTGGAGGA TTAGGAGAAG AAGCTGAATT TGTTGAAGTT GAGCCTGAAG CTAAACAGGA  240
AATTCTTGAA AACAAAGATG TGGTTGTTCA ACATGTTCAT TTTGATGGAC TTGGAAGGAC  300
TAAAGATGAT ATCATCATTT GTGAAATTGG AGATGTTTTC AAGGCCAAAA ACCTAATTGA  360
GGTAATGCGG AAATCTCATG AAGCCCGTGA AAAATTGCTC CGTCTTGGAA TTTTTAGACA  420
AGTGGATGTT TTGATTGACA CATGTCAAGG TGATGACGCA CTTCCAAATG GGTTAGACGT  480
TACCTTTGAA GTAACTGAAT TGAGGAGATT AACGGGCAGT TATAACACCA TGGTTGGAAA  540
CAATGAAGGC AGTATGGTAC TTGGCCTCAA GCTTCCTAAT CTTCTTGGTC GTGCAGAAAA  600
GGTGACCTTT CAGTTTTCCT ATGGAACAAA AGAAACTTCG TATGGCCTGT CCTTCTTCAA  660
ACCACGGCCC GGAAACTTCG AAAGAAATTT CTCTGTAAAC TTATATAAAG TTACTGGACA  720
GTTCCCTTGG AGCTCACTGC GGGAGACGGA CAGAGGAATG TCAGCTGAGT ACAGTTTTCC  780
CATATGGAAG ACCAGCCACA CTGTCAAGTG GGAAGGCGTA TGGCGAGAAC TGGGCTGCCT  840
CTCAAGGACG GCGTCATTTG CTGTTCGAAA AGAAAGCGGA CATTCACTGA AATCATCTCT  900
TTCGCACGCC ATGGTCATCG ATTCTCGGAA TTCTTCCATC TTACCAAGGA GAGGTGCTTT  960
GCTGAAAGTT AACCAGGAAC TGGCAGGCTA CACTGGCGGG GATGTGAGCT TCATCAAAGA 1020
AGATTTTGAA CTTCAGTTGA ACAAGCAACT CATATTTGAT TCAGTTTTTT CAGCGTCTTT 1080
CTGGGGCGGA ATGTTGGTAC CCATTGGTGA TAAGCCGTCA AGCATTGCTG ATAGGTTTTA 1140
CCTTGGGGGA CCCACAAGCG TCCGCGGATT CAGCATGCAC AGCATCGGGC CACAGAGCGA 1200
AGGAGACTAC CTAGGTGGAG AAGCGTACTG GGCCGGCGGC CTGCACCTCT ACACCCCATT 1260
ACCTTTCCGG CCAGGCCAGG GTGGCTTTGG AGAACTTTTC CGAACACACT TCTTTCTCAA 1320
CGCAGGAAAC CTCTGCAACC TCAACTATGG GGAGGGCCCC AAAGCTCATA TTCGTAAGCT 1380
GGCTGAGTGC ATCCGCTGGT CGTACGGGGC CGGGATTGTC CTCAGGCTTG GCAACATCGC 1440
TCGGTTGGAA CTTAATTACT GCGTCCCCAT GGGAGTACAG ACAGGCGACA GGATATGTGA 1500
TGGCGTCCAG TTTGGAGCTG GGATAAGGTT CCTGTAGCCG ACACCCCTAC AGGAGAAGCT 1560
CTGGGACTGG GGCAGCAGCA AGGCGCCCAT GCCACACACC GTCTCTCGAG GAAACGCGGT 1620
TCAGCGATTC TTTGACTGCG GACCCTGTGG GAAACCCCGT CAATAAATGT TAAAGACACA 1680
CTCAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1740
AAAAAAAAAA AAAAGGGGCG GCCGCCGACT AGTGACCTCT TCGCCC                1786
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